```
================================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Keisha Douglas
Timestamp: [year=2009; month=1; day=22; hr=16; min=26; sec=44; ms=514; ]
================================================================
```

```
****************************************************************
Reviewer Comments:
<210>   56

<211>   17752
<212>   DNA
<213>   Phaeodactylum tricornutum, Physcomitrella patens

<210>   71

<211>   17061
<212>   DNA
<213>   Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis
elegans


 The above <213> responses for sequence id#'s 56 and 71 are both
invalid, only one organism response is allowed for this line.

<210>   100
<211>   25
<212>   DNA
<213>   unknown



<220>
<221>   misc_feature
<222>   (1)..(25)
<223>   ACtrau-5'


<210>   103
```

```
<211>   22
<212>   DNA
<213>   unknown


<220>
<221>   misc_feature
<222>   (1)..(22)
<223>   YES-HIS-5'
```

 Please explain the above <223> responses for sequence id#s 100 and 103.
 FYI, please do not use foreign language in U.S. applications. Please
correct the remaining sequences showing similar errors.
 ****

Application No: 10552013   Version No: 2.0

Input Set:

Output Set:

Started:	2009-01-07 16:25:11.916
Finished:	2009-01-07 16:25:23.759
Elapsed:	0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings:	109
Total Errors:	51
No. of SeqIDs Defined:	148
Actual SeqID Count:	148

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)

```
        Input Set:


        Output Set:



        Started:    2009-01-07 16:25:11.916
       Finished:    2009-01-07 16:25:23.759
        Elapsed:    0 hr(s) 0 min(s) 11 sec(s) 843 ms
 Total Warnings:    109
   Total Errors:    51
No. of SeqIDs Defined:   148
 Actual SeqID Count:     148
```

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72) This error has occured more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (75)

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            Input Set:


           Output Set:



           Started:    2009-01-07 16:25:11.916
          Finished:    2009-01-07 16:25:23.759
           Elapsed:    0 hr(s) 0 min(s) 11 sec(s) 843 ms
    Total Warnings:    109
      Total Errors:    51
No. of SeqIDs Defined:  148
 Actual SeqID Count:    148
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Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75)
W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81) This error has occured more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916

Finished: 2009-01-07 16:25:23.759

Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms

Total Warnings: 109

Total Errors: 51

No. of SeqIDs Defined: 148

Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110>   Renz, Andreas
        Sozer, Nursen
        Frentzen, Margit
        Bauer, Jorg
        Keith, Stobart
        Fraser, Thomas
        Lazarus, Colin M
        Qi, Baoxiu
        Abbadi, Amine
        Heinz, Ernst

<120>   NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
        UNSATURATED FATTY ACIDS

<130>   13478-00002-US

<140>   10552013
<141>   2005-09-30

<150>   PCT/EP2004/003224
<151>   2004-03-26

<150>   DE103 14 759.4
<151>   2003-03-31

<150>   DE103 48 996.7
<151>   2003-10-17

<160>   148

<170>   PatentIn version 3.3

<210>   1
<211>   1047
<212>   DNA
<213>   Thraustochytrium

<220>
<221>   CDS
<222>   (38)..(952)
<223>   LPAAT

<400>   1

gggcggtgtc cggccgttcg agcgcgtgga cgccaac atg agc gcg tgg acg agg   55
                                        Met Ser Ala Trp Thr Arg
                                         1   5
gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg   103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
         10   15   20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc   151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
     25   30   35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc   199

```
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys
    40                  45                  50
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc     247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                  60                  65                  70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg     295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                75                  80                  85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac     343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                90                  95                  100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc     391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
        105                 110                 115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc     439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
    120                 125                 130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct     487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                 140                 145                 150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg     535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
                155                 160                 165
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag     583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
                170                 175                 180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag     631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
        185                 190                 195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg     679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
    200                 205                 210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac     727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                 220                 225                 230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag     775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                235                 240                 245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg     823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
                250                 255                 260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc     871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
        265                 270                 275
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga     919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
    280                 285                 290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca   972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                 300                 305
agcggtccag caacgggaga ttaaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa  1032
aaaaaaaaaa aaaaa                                                   1047


<210>   2

<211>   305
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<212> PRT

<213> Thraustochytrium

<400> 2

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Met Ser Ala Trp Thr Arg Ala Lys Thr Ala Val Gly Leu Leu Thr Leu
1               5                   10                  15
Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
            20                  25                  30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
        35                  40                  45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
    50                  55                  60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65                  70                  75                  80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
                85                  90                  95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
                100                 105                 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
            115                 120                 125
Ile Val Asp Arg Glu Gly Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
            130                 135                 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145                 150                 155                 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
                165                 170                 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
                180                 185                 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
            195                 200                 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
    210                 215                 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225                 230                 235                 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
                245                 250                 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260                 265                 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
    275                 280                 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
    290                 295                 300
Leu
305
```

<210> 3
<211> 1701

<212> DNA

<213> Physcomitrella patens

<220>
<221> misc_feature

<400> 3

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aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc   120
aactgaaaac ttgttttaat tttttcttaa attgaaattc tgtgcctgaa agccaactct   180
aggtccatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgct   240
tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg   300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag   360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt   420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat   480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc   540
cttgtttggt tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt   600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg   660
gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtaccc atccatggct   720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca   780
agtaaatcat acttgcttaa tgtacttagc aatttgtcat ttttgactta ttgtgatgta   840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga   900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact   960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag  1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt  1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg  1140
ctgtatgatc tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct  1200
ttccctgaca gtggaattga agagagccct ttgaacatag tggaaggtgt ttgcaatgtt  1260
gctctacacg tagtccttag cggttgggta ttctggtgct gtttcattc ggtttggttg  1320
aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga  1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt  1440
agttgtaatt ggtttgttta ttccgattcc aaagctgagt ttaaggtgtga ggctcctctt  1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta  1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt  1620
ctcctttacc catcttgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc  1680
cccaaaaaaa aaaaaaaaaa a                                            1701
```

<210> 4

<211> 714
<212> DNA

<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(714)
<223> LPAAT

<400> 4

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1               5                   10                  15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc    96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat   144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
```

```
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa        192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                      55                      60
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt        240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                      70                      75                      80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac        288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                    85                      90                      95
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta        336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100                     105                     110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca        384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
            115                     120                     125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat        432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
        130                     135                     140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca        480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                     150                     155                     160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg        528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165                     170                     175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta        576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
                180                     185                     190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc        624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
            195                     200                     205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa        672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
        210                     215                     220
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa              714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                     230                     235
```

<210> 5

<211> 237

<212> PRT

<213> Physcomitrella patens

<400> 5

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Met Ala Leu Met Tyr Ile Cys Asn Leu Leu Tyr Asn Leu His Leu Phe
1               5                   10                      15
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                      30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                      40                      45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                      55                      60
```

Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65   70   75   80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
                85   90   95
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
                100   105   110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
        115   120   125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
    130   135   140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145   150   155   160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                165   170   175
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
                180   185   190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195   200   205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
    210   215   220
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225   230   235

<210> 6

<211> 507

<212> DNA

<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 6

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accggactga tgctcagtct aggcaccatg cggctggcaa cgttcggcga agggctgtgg   120
acaatatgtg gtcccacgtc atgttgttcc cggagggcac taccaccaat ggcagagcaa   180
taatcgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta   240
gataccctca caagtatgtc aaccctctt ggtgtgacca aggaggtccg ttggtcgttg   300
tgttgcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga   360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga   420
tggctaaagc gttaggcatc gtgtgcacag aacacagctt tctggatatt aagctagcgc   480
tggctgcaga aaagctcaaa cagcctt   507

<210> 7

<211> 1566

<212> DNA
<213> Physcomitrella patens

<220>
<221> CDS
<222> (1)..(1566)

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atg gag agc aca gca gat gtc gga atg tcc gac gac gat cct atc ctt        48
Met Glu Ser Thr Ala Asp Val Gly Met Ser Asp Asp Asp Pro Ile Leu
1               5                   10                  15
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa        96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
                20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc       144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
        35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg       192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
    50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg       240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc       288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
                85                  90                  95
ggc gtc aca gat ccc ttg ttt aag
Gly Val Thr Asp Pro Leu Phe Lys
```